2014

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Summary

Purebred Red Angus genotypes, via the Ilumina BovineSNP50 assay, and expected progeny differences (EPD) were used to evaluate the accuracy of genomic predictors for traits that are currently reported through the American Red Angus Associations' National Cattle Evaluation. Two genomic predictors were evaluated, one derived using prediction equations from the National Beef Cattle Evaluation Consortium and the other from Zoetis.

Introduction

Several beef breed associations, including the American Angus Association, American Simmental Association, American Hereford Association, American Brahman Breeders Association (tenderness only), and the Red Angus Association of America, are currently augmenting their traditional expected progeny differences (EPD) with genomic information. In addition, many other breeds are nearing deployment of this technology. These genomic predictors, or molecular breeding values (MBV), are currently generated by multiple service providers including Zoetis (formally Pfizer) and GeneSeek, a Neogen Company. Many breeds utilize genomic prediction equations developed by the National Beef Cattle Evaluation Consortium (NBCEC) whereby they own the intellectual property arising from discovery of the genomic predictors. In either case, it has been clearly demonstrated that the inclusion of MBV into EPD can increases EPD accuracy particularly on unproven animals (i.e., yearling bulls). The magnitude of this change in accuracy is determined by the proportion of genetic variation explained by the MBV. Consequently, the objective of the current study was to evaluate the efficacy of two different MBV in Red Angus cattle.

Procedure

Red Angus specific genomic predictors were evaluated using EPD, Beef Improvement Federation accuracies, and MBV provided by the Red Angus Association of America for genotyped animals (n = 233) not used in training of the MBV. For each trait, there were two different prediction equations used to derive the MBV: one from Iowa State University and the National Beef Cattle Evaluation Consortium (NBCEC), and the other from Zoetis. The two training populations differed in the specific animals used, in the number of animals used, and the statistical model used. However, there was likely a considerable degree of overlap between the two training populations. Both MBV were evaluated if a MBV and corresponding EPD existed. The EPD were transformed by deregressing them and weighting them following the methods of Garrick and others (Genetics Selection Evolution, 2009). Beef Improvement Federation accuracies were transformed into the reliabilities used in the weighting of the deregressed EPD. The unweighted heritability of the deregressed EPD was set to an arbitrary value (0.4). To check that the final results were not sensitive to the choice of heritability, the analysis was rerun at different values of heritability and, as expected, the same results were obtained each time. A four-generation pedigree was constructed for the genotyped animals used in the evaluation. A two-trait linear mixed model was fitted using ASReml. The dependent variables were the MBV and weighted deregressed EPD. The model for the MBV included a fixed effect for the intercept, a random additive genetic effect, and a residual with variance fixed at 0.0001% of the unweighted phenotypic variance of the deregressed EPD. The model for the deregressed EPD included a fixed effect for the intercept, a random additive genetic effect, and a weighted random residual. The additive genetic and unweighted residual variances for the deregressed EPD were fixed at 0.4 and 0.6 of the deregressed unweighted phenotypic variance of the EPD, respectively. Any deregressed EPD with a reliability less than 0.1 was removed prior to analysis. The analysis was rerun without this edit and the results were very similar.

Results

In general, genetic correlations between the MBV and the trait of interest were moderate to high and would be expected to add accuracy to EPD for unproven animals. Genetic correlations and corresponding standard errors for continuous traits for the two MBV are detailed in Table 1. Differences between the two MBV (NBCEC and Zoetis) were small, although the NBCEC MBV had numerically higher genetic correlations with the trait of interest for all traits evaluated. This could be a function of the number of animals used in the training set or the relationship between the training data and the evaluation data or a function of both. Table 2 details the genetic correlations for threshold traits when the MBV were trained and evaluated using EPD either on the observed or underlying scale (NBCEC only). The genetic correlations for threshold traits were moderate to high, but differences did exist between estimates depending on the scale (observed or underlying) of the deregressed EPD used for training. The larger estimates of the genetic correlations may due to the nonlinear transformation of the EPD to the observed scale not being consistent with the assumptions of the model used to estimate the EPD. The moderate to high genetic correlations for threshold traits may be due to biases created by

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a combination of the relative low accuracies of EPD for threshold traits and the correlations in the prediction errors of the deregressed EPD.

Implications

Both MBV evaluated here have the potential to increase the EPD accuracy of unproven animals. Differences did exist between the two MBV, likely due to the animals used in training, both in terms of the number of animals and their relationship with the animals used in the evaluation data. The most critical differences existed for threshold traits. Differences did exist when genetic correlations between MBV and the trait of interest were estimated on the observed versus the underlying scale. For inclusion of MBV in national cattle evaluation, the theoretically sound method would include training MBV for threshold traits using deregressed EPD on the underlying scale.

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Table 1. Genetic correlations for continuous variation traits in Red Angus cattle with standard errors.

Trait	N	NBCEC Prediction Genetic Correlation	SE	Zoetis Prediction Genetic Correlation	SE
Birth Weight	197	0.644	0.053	0.586	0.058
Carcass Weight	199	0.661	0.065	0.528	0.075
Fat	166	0.488	0.098	0.429	0.099
Milk	192	0.399	0.085	0.319	0.087
Marbling	189	0.608	0.101	0.504	0.108
Ribeye Area	187	0.500	0.114	0.478	0.116
Weaning Weight	200	0.546	0.063	0.485	0.068
Yield Grade	190	0.382	0.114	—	—
Yearling Weight	200	0.579	0.061	0.449	0.071
Maintenance Energy	181	0.581	0.061	—	—

Table 2. Genetic correlations (standard errors) for threshold traits in Red Angus cattle.

Trait	N	NBCEC Prediction Observed Scale Genetic Correlation	NBCEC Prediction Underlying Scale Genetic Correlation
Calving Ease Maternal	170	0.458	0.679 (0.058)
Calving Ease Direct	176	0.479	0.588 (0.067)
Heifer Pregnancy	64	0.616	0.610 (0.124)
Stayability	104	0.801	0.787 (0.118)